Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	5	udp-Glc dehydrogenase	USPAT	ADJ	ON	2004/06/21 14:26
L2	26	hyaluron$ with (molecular weight distribution)	USPAT	ADJ	ON	2004/06/21 14:27
S1	5	udp-Glc dehydrogenase	USPAT	ADJ	ON	2004/06/07 16:42
S2	6662	amino acid WITH pharmaceut$	USPAT	ADJ	ON	2004/06/07 16:47
S3	1	pharmaceutical composition near("10") amino acid	USPAT	ADJ	ON	2004/06/07 16:47

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  * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 15:20:03 ON 21 JUN 2004

=> file biosis
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.21       0.21

FILE 'BIOSIS' ENTERED AT 15:20:17 ON 21 JUN 2004
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FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 16 June 2004 (20040616/ED)

FILE RELOADED: 19 October 2003.

=> s (udp (w) glc (w) dehydrogenase) (10a) (gene or express? or recombinan?)
         12602 UDP
          9936 GLC
        128518 DEHYDROGENASE
        884452 GENE
       1026727 EXPRESS?
        178608 RECOMBINAN?
L1           0 (UDP (W) GLC (W) DEHYDROGENASE) (10A) (GENE OR EXPRESS? OR RECOM
               BINAN?)

=>  s (udp (w) glc (w) dehydrogenase) (p) (gene or express? or recombinan?)
         12602 UDP
          9936 GLC
        128518 DEHYDROGENASE
        884452 GENE
       1026727 EXPRESS?
        178608 RECOMBINAN?
L2           3 (UDP (W) GLC (W) DEHYDROGENASE) (P) (GENE OR EXPRESS? OR RECOMBI
               NAN?)

=> d l2 bib ab 1-3

L2   ANSWER 1 OF 3  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2002:189016  BIOSIS
DN   PREV200200189016
TI   Characterization of the Streptococcus pneumoniae type 3 synthase.
AU   Cartee, R. T. [Reprint author]; Forsee, T. [Reprint author]; Yother, J.
     [Reprint author]
CS   University of Alabama at Birmingham, Birmingham, AL, USA
SO   Abstracts of the General Meeting of the American Society for Microbiology,
     (2001) Vol. 101, pp. 142-143. print.
     Meeting Info.: 101st General Meeting of the American Society for
     Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society for
     Microbiology.
     ISSN: 1060-2011.
DT   Conference; (Meeting)
     Conference; Abstract; (Meeting Abstract)
     Conference; (Meeting Poster)
LA   English
ED   Entered STN: 13 Mar 2002
     Last Updated on STN: 13 Mar 2002
AB   Type 3 polysaccharide is composed of the repeating unit -3) beta-D-GlcUA
     (1-4) beta-D-Glc (1- and is one of 90 different capsular polysaccharides
     identified in the gram positive pathogen Streptococcus pneumoniae.
     Synthesis of type 3 polysaccharide requires a single glycoslytransferase,
     the type 3 synthase.  This enzyme utilizes UDP-Glc and UDP-GlcUA to
     alternately add Glc and GlcUA to the nonreducing end of the polysaccharide
     chain.  When enzyme-polysaccharide complexes were incubated with a single
     substrate, 50-60% of the nascent polysaccharide chains were released from
     the enzyme.  In S. pneumoniae, once the nascent chain was released from
     the synthase, the enzyme was not capable of reinitiating synthesis
     suggesting that a primer was required.    ***Expression***   of the type 3
     synthase in Escherichia coli demonstrated, however, that the synthase was
     capable of reinitiating synthesis by utilizing a glycolipid present in E.
     coli membranes.  To determine if a primer was involved in initiation of
     type 3 polysaccharide synthesis in S. pneumoniae, we utilized a
     nonencapsulated type 3 strain that contains a nonsense mutation in the
       ***UDP***  -  ***Glc***     ***dehydrogenase***  .  The type 3 synthase
     from this strain facilitates examination of the initiation event because
     it lacks preformed type 3 polysaccharide due to the inability to
     synthesize UDP-GlcUA.  Although a primer has not yet been identified using
     this strain, we observed that the strain produced lower levels of the
     synthase and had 17% of the synthase activity as the parent strain.
     Additionally, polysaccharide synthesized in this strain was not released
     from the enzyme when incubated with a single substrate indicating that
     mutations in the   ***UDP***  -  ***Glc***     ***dehydrogenase***   were
     affecting not only synthase levels but also the activity of the enzyme.
     Examination of other S. pneumoniae strains with mutations in enzymes
     involved in forming type 3 polysaccharide precursors also showed a similar
     reduction in synthase levels and activity.  By exploring differences in
     type 3 synthase activity in both E. coli and mutant strains of type 3 S.
     pneumoniae, we are gaining new information regarding the mechanism of type
     3 polysaccharide synthesis.

L2   ANSWER 2 OF 3  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1997:251441  BIOSIS
DN   PREV199799550644
TI   A functional analysis of the Streptococcus pneumoniae genes involved in
     the synthesis of type 1 and type 3 capsular polysaccharides.
AU   Garcia, Ernesto [Reprint author]; Arrecubieta, Carlos; Munoz, Rosario;
     Mollerach, Marta; Lopez, Rubens
CS   Dep. Microbiol. Molecular, Centro Investigaciones Biol., Consejo Superior
     Investigaciones Cientificas, Velazquez 144, 28006 Madrid, Spain
SO   Microbial Drug Resistance, (1997) Vol. 3, No. 1, pp. 73-88.
     ISSN: 1076-6294.
DT   Article
     General Review; (Literature Review)
LA   English
ED   Entered STN: 13 Jun 1997
     Last Updated on STN: 13 Jun 1997
AB   Type 3 pneumococci produce a capsule composed of cellobiuronic acid units
     connected in a beta(1 fwdarw 3) linkage.  Cellobiuronic acid is a
     disaccharide consisting of D-glucuronic acid (GlcA) beta(1 fwdarw 4)
     linked to D-glucose (Glc).  The genes implicated in the biosynthesis of
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the type 3 capsule have been cloned, ***expressed*** , and biochemically characterized. The three type 3-specific genes-designated as cap3ABC-are transcribed together. However, the two complete open reading frames located upstream of cap3A are not transcribed and, consequently, are not required for capsule formation. The promoter of the cap3 operon was localized by primer extension analysis. The products of cap3A, cap3B, and cap3C were biochemically characterized as a ***UDP*** - ***Glc*** ***dehydrogenase*** , the type 3 polysaccharide synthase, and a Glc-1-P uridyltransferase, respectively. The Cap3B synthase was ***expressed*** in Escherichia coli, and pneumococcal type 3 polysaccharide was synthesized in this heterologous system. When a ***recombinant*** plasmid (pLSE3B) containing cap3B was introduced by transformation into encapsulated pneumococci of types 1, 2, 5, or 8, the lincomycin-resistant transformants displayed a binary type of capsule, this is, they showed a type 3 capsule in addition to that of the recipient type. Unencapsulated (S2) laboratory strains of S. pneumoniae also synthesized a type 3 capsule when transformed with pLSE3B. On the other hand, we have cloned and sequenced seven type 1-specific genes (designated as cap1A-G), and their functions have been preliminarily assigned based on sequence similarities.

L2 ANSWER 3 OF 3 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1993:499119 BIOSIS
DN PREV199396123126
TI Molecular cloning, identification, and sequence of the hyaluronan synthase gene from Group A Streptococcus pyogenes.
AU Deangelis, Paul L.; Papaconstantinou, John; Weigel, Paul H. [Reprint author]
CS Dep. Human Biol. Chem. Genetics, Univ. Tex. Med. Branch, Galveston, TX 77555-0647, USA
SO Journal of Biological Chemistry, (1993) Vol. 268, No. 26, pp. 19181-19184. CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
OS Genbank-L20853
ED Entered STN: 5 Nov 1993
Last Updated on STN: 13 Jan 1994
AB The hyaluronan (HA) synthase of Group A Streptococci has been identified by transposon mutagenesis and deletion analysis. The genes for the HA synthase and a recently identified ***UDP*** - ***Glc*** ***dehydrogenase*** (Dougherty, B. A., and van de Rijn, I. (1993) J. Biol. Chem. 268, 71187124) reside on a contiguous stretch of 3.2-kilobase pair DNA that can direct HA biosynthesis in Enterococcus faecalis and Escherichia coli as well as mutant Streptococcus (DeAngelis, P. L., Papaconstantinou, J., and Weigel, P. H. (1993) J. Biol. Chem. 268, 14568-14571). The synthase contains 395 residues (calculated M-r = 45,063) and migrates on SDS-PAGE with a molecular mass of 42 kDa. E. coli K5, which synthesizes UDP-glucuronic acid for production of its endogenous capsular polysaccharide, can make HA if it contains a plasmid encoding the intact 42-kDa protein. E. coli SURE or chi-1448 cells containing the same construct, however, cannot produce HA since these strains cannot make both required sugar nucleotide precursors. The HA synthase is predicted to be an integral membrane protein with four membrane-associated helices, which is consistent with the location of the enzyme activity in Streptococci. There is significant homology between the HA synthase and the Rhizobium nodC ***gene*** product, an enzyme that synthesizes chitin-like oligomers. This is the first description at the molecular level of an enzyme shown to synthesize a glycosaminoglycan.

=> log h

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	9.70	9.91

SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 15:22:24 ON 21 JUN 2004